

Figure 1.

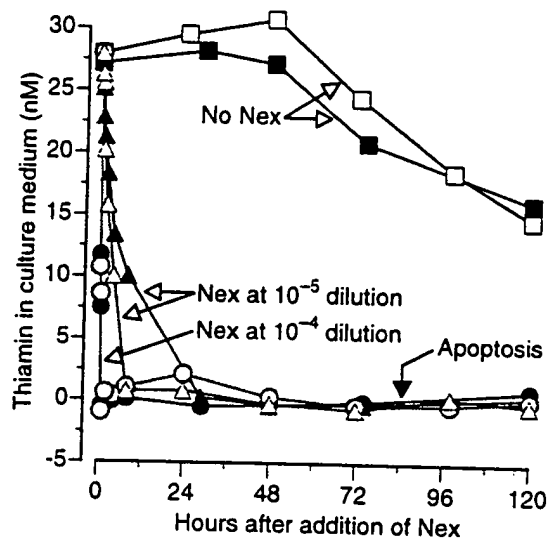


Figure 2.

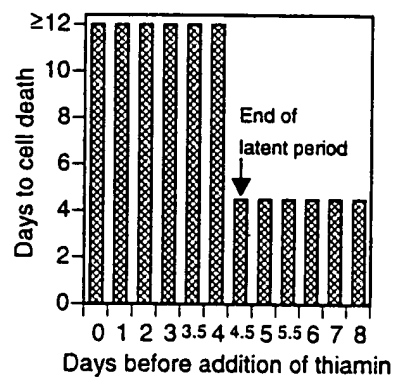


Figure 3.

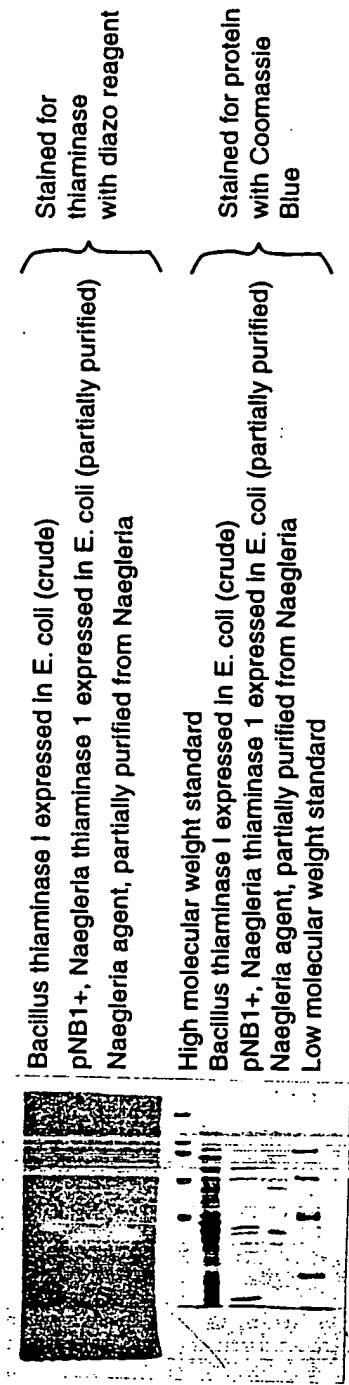


Figure 4.

(SEQ ID NO: 1)

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1   ATGTCCACTC AACCAAAGAC ACTCACTGTT GGTCTCTTCC CATATCTTCC TTCTTGGAAT
61  GAAAATGGCA ACGAAGTTAA ATTGATCAAT TTGATCAAGG ATGTTTTGCC AACTCAGGTT
121 TCCGGATATA ATATCGAATA TACCGAATTT GATTGTTACA GTGATGCTAG TCTTCAAAGT
181 CTTCCAGATG TTTTCTCAAC TGATAGCATT TTCCTTCCAT ATCTTGTTTC TTTGGGTGGT
241 GTCAAGAGTT TGGATGAATC ATTGGTTTCGTT GGTGTTACTG GTGATTTGCA TAGTTTTGTT
301 TCCTCAAGTG CCTCTGTCAA TGGTTCCGTT TATGGTTTCC CACAATACTT GTGCTCAAAC
361 TTTTATTGT CCTCACCAA TGGTACTCAA CAAGCATCTT CCCTTTTAGA ATTGGCTCAA
421 AAGGTTGGTT ATGAACAAAT TGTTTATCCA GATGTTGCCT CTTCTAGTTC TTTCACAGTT
481 TCCGATTGTT ATCAACAATT ACTCCAATCA TCATCATCAG CTGCAGTTGA TATCAAGGCC
541 TCTGATCTTC CACAATCTGG TGACCAAGTC AACAAGGATA TCACTCAAAA ATATAGAACC
601 ATTTTGGATT CAACAGTTGT TGCCTCTCAA AGAGAATATA TTAAGTCTGT AAAGCAAGGT
661 AAACCAATTT CAAACTACTA TGTCGGATAT AGTGAAAGTA TGTGTGAAAT TAAGGATATC
721 ATCAGAGATC AACAATACAA TGTTCAACTC ATTGGTACCT CTGATAAGCC ATACGTTTAT
781 ACTGATGTTT TGGCTTTGAA TTCCAATTTG TGTGATGAAA AGCAAAAGGT TGCTGTTGAA
841 GTTATCAAGA ATTTATTGAC TAATACTTTA GTTTTGGACT TGTGAGGCTC CGGATTAAGT
901 CTCCCAGCCA ACAAGAATGG TATTGCTCAT TTGGCTAAAT CATCAAACCT TTATGCTCAA
961 TTGAGCCAAC AATTCGATGC CAAGGAAAGT GAAGTTAGAG TTTTGAGATG TGTTGACTTT
1021 GCTAACCAAG AAGTTAAGAA TTGTGCTGGT GTCTTGAGAC CATTCTTCA ACATATTGCT
1081 GTTGCTACTT TGCCTTGTTC GACTGCTGAC ACTGTGAAA AGGCTAAGAG TGGTCACCCT
1141 GGTATGCCAA TTGGTATGTC ACCAATTGCC TATGTTTTGT GGAAGTTCTT CTTCAAATCA
1201 TCTAAGGATG ATGTCAATTG GTTGAACAGA GATAGATTGT TTTTGAGTAA TGGTCACGGT
1261 TGACATTGC TTTATGCCAT GTTGCACCTC ACTGATTGTA ACTTGAGTTT GGATGATCTC
1321 AAGAATTTCA GAAGTTTGCA TTCCAAGACT CCTGGTCACC CAGAATATGG TCACACTGAA
1381 GGTGTTGATG CTACTACTGG TCCATTGGGT CAAGGTGTTT GTAATGCTAT TGGTATGGCT
1441 CTCTCTGAAG CTCACCTGGC TGCTCGTTTC AATAAGGATG GACAAAATAT CTTTGATCAC
1501 CACACCTATG TTTTCCTTGG TGATGGTTGT TTGATGGAAC GTGTTGCTAT GGAAGGTCTC
1561 TCATTTGCTG GTCACCAAAA GTTGAACAGT TTGATTGTTT TCTATGATGA CAATAGTATT
1621 ACTATTGATG GTAAGACTGA ATTGACCTTT ACTCAAAATA CTCCAGAAGT CATGAGAGGT
1661 TTTGGATGGC ACGTAATTGT TGTCGACAAG GCTGATAATG ACTTGGTTGG TATTAAGGAA
1721 GCTATTTTGG AAGCTCACAC TGTTACTGAC AAGCCAATCA TGATCGTTTG TAAGACTACA
1781 ATTGGTTATT CCTCAAAGGT TCAAGGTACT GCTAAGGTTT ACGGTTCTCC ATTGGGTGCT
1841 GATGGATTGA AGAATTTGAA GGAACTTGT GGTTCCTACT GTAATGATT CTTCCATGTT
1901 CCAGAAATTG TCAGAAAGGA CTTTGCTACT GTCATTAATA GAAATAGTGA AAAGCTCTCT
1961 CAATGGAAGC AAGTTAAATC TGCCTATGAT ACCACTCATG CTACTGAATC CCAACTCTCT
2021 CAAAGAATGA TTAATCACGA ATTGGAAGGT GATGTTATGG AAAAGTTGCC AAAATACCTC
2081 GAACAAAAGA AGATTGCTAC CAGATCTACA TCTCAACAAG TTTTGAATGC CATCTATCCA
2141 CTCATTCTTT CTCTCGTTGG TGGTTCAGCT GACTTGACTC CATCCAACCT GACTGATGTA
2201 ACTGGATGTC AAGATTTCCA ACCAAACAAT AGAGTTGGTA GATATATCAG ATTTGGTGTC
2261 CGTGAACATG CCAATGGTTGC TATTGCCAAT GGTATTCTCT ATCATGGTGT TCTTAGAACC
2321 TATGTTGGTA CATTCTTGAA CTTTGCTTCA TATGCTTTGG GTGCTATCAG ATTGAGTGCC
2381 TTGTCTGGTC TTCCAAATAT TTATGTTTTT ACTCATGACA GTATTGGTCT TGGTCAAGAT
2441 GGTCCAATC ACCAACCTGT TGAAGTTTGA CCAATGTTGA TAGCCATTCC AAATCACATT
2521 GTTTTCAGAC CTGCTGATGG TAGAGAAACC AGTGGTGCTT ATTTGTGGGC TGTTCAATCA
2581 AAGAAGACTC CATCCTCAAT GATTCTTTCT CGTCAAGATT TGCCACAATT GACTGGTACT
2641 GATATTTCAA AGGTTGCTTT GGGTGCCTAT GTTATCCAAG GTGATGCTAC TCCTGATGTT
2701 GTCCTTGTTG GACTGTTTTC TGAAGTTTCC CTCATGGTTG AAGCTGCTGA AAGTTGAAG
2761 GCTAACCTTA AGGTTAACGT GTTTTCCATG CCAAGTTGGG AATTGTTTGT TCGTCAATCA
2821 GAAGAATACA GGAAGACTGT CTTCCCAGAT GGTATTCCAG TTGTCAGTGC CGAAGCTTCA
2881 TCAACCTTTG GTTGGACAAG CTTTGCTCAC TATGCTGTTG GTATGACTAC TTTCCGTGCT
2941 AGTGCTGCTG CTGAAGAAGT TTACAAACTC CTCAAGATTA CCTCAGACAA TGTTGCTGAA
3001 AAGGCCACCA AATTGGTTAC CAAGTATGGT AAGCAAGCTC CAAGACTCAG CTTGTCTCTT
3061 GTTGGTGAAG AACTCTAA

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Figure 5.

(SEQ ID NO: 2)

MSTQPKTLTVGLFPYLPSPWNENGNEVKLINLIKDVLPQTQVSGYNIEYTEFDCYSDASLQSLPDVFSTDSIFLPYLVSLGG  
VKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPPQYLCNFFLLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFTV  
FGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYYVGYSESMCEIKDI  
IRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKVAVEVIKNLLTNTLVLDLLGLGLTLPANKNGIAHLAKSSNFYAQ  
LSQQFDAKESEVRVLRVDFANKEVKNCAGVLRPFLQHIAVATLRCLTADTVEKAKSGHPGMPIGMSPIAYVLWKFFFKS  
SKDDVNWLNRRDRFVLSNGHGCTLLYAMLHLTDCNLSLDDLKNFRSLHSKTPGHPEYGHTEGVDATTGPLGQGVCAIGMA  
LSEAHLAARFNKDGQNI FDHHTYVFLGDGCLMERVAMEGLSFAGHQKLNKLIVFYDDNSITIDGKTELTFTQNTPEVMRG  
FGWHVIVVDKADNDLVGIKEAILEAHTVTDKPIMIVCKTTIGYSSKVQGTAKVHGSPLGADGLKNLKETCGFTGNDFFHV  
PEIVRKDFATVINRNSEKLSQWKQVK SAYDTTHATESQLLQRMINHELEGDVMEKLPKYLEQKKIATRSTSQQVLNAIYP  
LIPSLVGG SADLTPSNLT DVTGCQDFQPNNRVGRYIRFGVREHAMVAIANGILYHGVLRTYVGTFLNFASYALGAIRLSA  
LSGLPNIIYVFTHDSIGLGQDGPTHQPVEVLPMLIAIPNHIVFRPADGRETS GAYLWAVQSKKTPSSMILSRQDL PQLTGT  
DISKVALGAYVIQGDATPDVVLVGTGSEVSLMVEAAEKLKANLKVNVVSMPSWELFVRQSEYRKTVPDGPVVS AEAS  
STFGWTSFAHYAVGMTTFGASAAAEVYKLLKITS DNVAEKATKLVTKYGKQAPRLSLSLVGEEL

Figure 6.

(SEQ ID NO: 3)

ATGTCCACTCAACCAAGACACTCACTGTTGGTCTCTTCCCATATCTTCTTCTTGAATGAAAATGGCAACGAAGTTAA  
ATTGATCAATTTGATCAAGGATGTTTTGCCAACTCAGGTTTCCGGATATAATATCGAATATACCGAATTTGATTGTTACA  
GTGATGCTAGTCTTCAAAGTCTTCCAGATGTTTTCTCAACTGATAGCATTTTCCTTCCATATCTTGTTTCTTTGGGTGGT  
GTCAAGAGTTTGGATGAATCATTGGTTCGTGGTGTACTGGTGATTGTCATAGTTTTGTTTCTCAAGTGCCTCTGTCAA  
TGGTTCGTTTATGGTTTCCCACTACTTGTGCTCAAACCTTTTTATTGTCCTCACCAAATGGTACTCAACAAGCATCTT  
CCCTTTTAGAATTGGCTCAAAAGGTGGTTATGAACAAATTGTTTATCCAGATGTTGCCTCTTCTAGTTCTTTCACAGTT  
TTCGGATTGTATCAACAATTACTCCAATCATCATCATCAGCTGCAGTTGATATCAAGGCCTCTGATCTTCCACAATCTGG  
TGACCAAGTCAACAAGGATATCACTCAAAAATATAGAACCATTTTGGATTCAACAGTTGTTGCCTCTCAAAGAGAATATA  
TTAACTCTGTAAAGCAAGGTAAACCAATTTCAAACCTACTATGTCGGATATAGTGAAAGTATGTGTGAAATTAAGGATATC  
ATCAGAGATCAACAATACAATGTTCAACTCATTGGTACCTCTGATAAGCCATACGTTTATACTGATGTTTTGGCTTTGAA  
TTCCAATTTGTGTGATGAAAAGCAAAAGGTGCTGTTGAAGTTATCAAGAATTTATTGACTAATACTTTAGTTTTGGACT  
TGTTGGGTCTCGGATTAACTCTCCAGCCAACAAGAATGGTATTGCTCATTGGCTAAATCATCAAACCTTTTATGCTCAA  
TTGAGCCAACAATTCGATGCCAAGGAAAGTGAAGTTAGAGTTTTGAGATGTGTTGACTTTGCTAACAAGGAAGTTAAGAA  
TTGTGCTGGTGTCTTGAGACCATTTCCTT

Figure 7. (SEQ ID NO: 3/SEQ ID NO: 4)

1/1 31/11  
 ATG TCC ACT CAA CCA AAG ACA CTC ACT GTT GGT CTC TTC CCA TAT CTT CCT TCT TGG AAT  
 Met ser thr gln pro lys thr leu thr val gly leu phe pro tyr leu pro ser trp asn

61/21 91/31  
 GAA AAT GGC AAC GAA GTT AAA TTG ATC AAT TTG ATC AAG GAT GTT TTG CCA ACT CAG GTT  
 glu asn gly asn glu val lys leu ile asn leu ile lys asp val leu pro thr gln val

121/41 151/51  
 TCC GGA TAT AAT ATC GAA TAT ACC GAA TTT GAT TGT TAC AGT GAT GCT AGT CTT CAA AGT  
 ser gly tyr asn ile glu tyr thr glu phe asp cys tyr ser asp ala ser leu gln ser

181/61 211/71  
 CTT CCA GAT GTT TTC TCA ACT GAT AGC ATT TTC CTT CCA TAT CTT GTT TCT TTG GGT GGT  
 leu pro asp val phe ser thr asp ser ile phe leu pro tyr leu val ser leu gly gly

241/81 271/91  
 GTC AAG AGT TTG GAT GAA TCA TTG GTT CGT GGT GTT ACT GGT GAT TTG CAT AGT TTT GTT  
 val lys ser leu asp glu ser leu val arg gly val thr gly asp leu his ser phe val

301/101 331/111  
 TCC TCA AGT GCC TCT GTC AAT GGT TCC GTT TAT GGT TTC CCA CAA TAC TTG TGC TCA AAC  
 ser ser ser ala ser val asn gly ser val tyr gly phe pro gln tyr leu cys ser asn

361/121 391/131  
 TTT TTA TTG TCC TCA CCA AAT GGT ACT CAA CAA GCA TCT TCC CTT TTA GAA TTG GCT CAA  
 phe leu leu ser ser pro asn gly thr gln gln ala ser ser leu leu glu leu ala gln

421/141 451/151  
 AAG GTT GGT TAT GAA CAA ATT GTT TAT CCA GAT GTT GCC TCT TCT AGT TCT TTC ACA GTT  
 lys val gly tyr glu gln ile val tyr pro asp val ala ser ser ser ser phe thr val

481/161 511/171  
 TTC GGA TTG TAT CAA CAA TTA CTC CAA TCA TCA GCT GCA GTT GAT ATC AAG GCC  
 phe gly leu tyr gln gln leu leu gln ser ser ser ala ala val asp ile lys ala

541/181 571/191  
 TCT GAT CTT CCA CAA TCT GGT GAC CAA GTC AAC AAG GAT ATC ACT CAA AAA TAT AGA ACC  
 ser asp leu pro gln ser gly asp gln val asn lys asp ile thr gln lys tyr arg thr

601/201 631/211  
 ATT TTG GAT TCA ACA GTT GTT GCC TCT CAA AGA GAA TAT ATT AAC TCT GTA AAG CAA GGT  
 ile leu asp ser thr val val ala ser gln arg glu tyr ile asn ser val lys gln gly

661/221 691/231  
 AAA CCA ATT TCA AAC TAC TAT GTC GGA TAT AGT GAA AGT ATG TGT GAA ATT AAG GAT ATC  
 lys pro ile ser asn tyr tyr val gly tyr ser glu ser met cys glu ile lys asp ile

721/241 751/251  
 ATC AGA GAT CAA CAA TAC AAT GTT CAA CTC ATT GGT ACC TCT GAT AAG CCA TAC GTT TAT  
 ile arg asp gln gln tyr asn val gln leu ile gly thr ser asp lys pro tyr val tyr

781/261 811/271  
 ACT GAT GTT TTG GCT TTG AAT TCC AAT TTG TGT GAT GAA AAG CAA AAG GTT GCT GTT GAA  
 thr asp val leu ala leu asn ser asn leu cys asp glu lys gln lys val ala val glu

841/281 871/291  
 GTT ATC AAG AAT TTA TTG ACT AAT ACT TTA GTT TTG GAC TTG TTG GGT CTC GGA TTA ACT  
 val ile lys asn leu leu thr asn thr leu val leu asp leu leu gly leu gly leu thr 1

901/301 931/311  
 CTC CCA GCC AAC AAG AAT GGT ATT GCT CAT TTG GCT AAA TCA TCA AAC TTT TAT GCT CAA  
 leu pro ala asn lys asn gly ile ala his leu ala lys ser ser asn phe tyr ala gln

961/321 991/331  
 TTG AGC CAA CAA TTC GAT GCC AAG GAA AGT GAA GTT AGA GTT TTG AGA TGT GTT GAC TTT  
 leu ser gln gln phe asp ala lys glu ser glu val arg val leu arg cys val asp phe

1021/341 1051/351  
 GCT AAC AAG GAA GTT AAG AAT TGT GCT GGT GTC TTG AGA CCA TTC CTT  
 ala asn lys glu val lys asn cys ala gly val leu arg pro phe leu

Figure 8-1.

Abbrev.	Genbank	Enzyme and Organism
ScTKT1ct	- P23254	Transketolase of <i>Saccharomyces cerevisiae</i>
CpTKT7ct	- Q42677	Transketolase of <i>Craterostigma plantagineum</i>
EcTKT2ct	- P33570	Transketolase of <i>Escherichia coli</i>
BsTKTct	- P45694	Transketolase of <i>Bacillus subtilis</i>
MgTKT	- P47312	Transketolase of <i>Mycoplasma genitalium</i>
MjPTK1	- Q58092	Transketolase of <i>Methanococcus jannaschii</i>
BSTP	- P45741	Thiaminase I precursor from <i>Bacillus thiaminolyticus</i>
N40KAT	- ----->	Thiaminase I of <i>Naegleria gruberi</i> , aa 1-356

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ScTKT1ct  ADDVK---QLKSKFGFNPDKSFVVPQEVYD-HYQKTILKPGVEANNKWNKLFSEYQKKFP  56
CpTKT7ct  PKEAE---ATRKNLGW-PYEPFHPDDVKK-HWSRHIAE-GAALESANNAKFAEFQKKFP
EcTKT2ct  EEEVA---LARQKLGW-HHPPFEIPKEIY--HAWDAREK-GEKAQSWNEKFAAYKKAHP
BsTKTct   KEESK---LTKEAYAWTYEEDFYVPSEVYE-HFAVAVKESGEKKEQEWNAQFAKYKEVYP
MgTKT     EVDFQ---LFEKRTNT-NFNFFNYPDSIYH-WFKQTVIERQKQIKEDYNLLISLKD-K-P
MjPTK1    -----
BsTP      MSKVKGFIYKPLMVMLALLLVVSPAGAGAAHSDASSDITLKVAIYPYVPDPAFQAQAVL
N40KAT     MSTQP----KTLTVGLFPYL----PS-----WNENGNEVKLINLIKDVLP-----

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ScTKT1ct  ELGAELARRLSGQLPANWESKLPTYTAKDSA----VATRKLSSETVLEDVYNQLPELIGGS  112
CpTKT7ct  EEAADLKSIIITGELPTNWESIFPTYTPENPG----LPTRTLSHQILNGLGDVLPGLLGGS
EcTKT2ct  QLAEETFRRMSGGLPKDWEKTQKYINELQANPAKIATRKASQNTLNAYGPMPELLGGS
BsTKTct   ELAEQLELAIKGELPKDWDQEVVPYE-KGSS----LASRASSGEVLNGLAKKIPFFVGGS
MgTKT     -LFFKFTNWIDSDFQALYLNQLDEKKVAKD----SATRNYLKDFLNQINNPNNSNLYCLN
MjPTK1    -----MVKLSGVYKG-----MRKGYGETLIELGKKYENLVVLD
BsTP      DQWQRQEPGVKLEF-TDWDYSADPPDDLVDV----FVLDSIFLSHFVDAGYLLP-FGSQD
N40KAT     -----QVSGYNIEY-TEFDCYSDASLQSLPD---VFSTDSIFLPYLVSLGGVKSLESLV

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ScTKT1ct  ADLTPSNLTRWKEALDFQPPSSSGSGNYSGRYIRYGIREHAMGA---IMNGISAFGANYKPYGG  172
CpTKT7ct  ADLTLNMAFLKNSGDFQKKSPGE-----RNVKFGAREHAMGS---ICNGLALHSPGLLPYCA
EcTKT2ct  ADLAPSNLTIWKGSVSLKEDPAGN-----YIHVGVREFGMTA---IANGIAHHG-GFVPTYA
BsTKTct   ADLAGSNKTTIKNAGDFTAVDYSG-----KNFWFGVREFAMGA---ALNGMALHG-GLRVFGG
MgTKT     ADVSRS--CFIKIGDDNLHENPCS-----RNIQIGIREFAMAT---IMNGMALHG-GIKVMGG
MjPTK1    ADLSGS-----TQTAMFAKEFPE-----RFFNAGVAEQNMIG---MAAGLATTG--KIVFAS
BsTP      IDQAEDVLPFALQGAKRNGEVYGLP-----QILCTNLLFYRKGDLDKIGQVDNIYELYKKIG
N40KAT     RGVGTGLHSFVSSSASVNGSVYGFPP-----QYLCNFFLLSS----PNGTQQAS-SLLELAQ

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\*  
Catalytic Cys

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ScTKT1ct  TFLNFVS-YAAGAVR-LSALSGHPVIWVATHDSIGV-GE---DG-PTHQPIET--LAHF  222
CpTKT7ct  TYFVFTD-YMRAAMR-ISALSKARVLYIMTHDSIGL-GE---DG-PTHQPVEH--LASF
EcTKT2ct  TFLMFVE-YARNAAR-MAALMKARQIMVYTHDSIGL-GE---DG-PTHQAVEQ--LASL
BsTKTct   TFFVFSD-YLRPAIR-LAALMGLPVTVYVTHDSIAV-GE---DG-PTHEPVEQ--LASL
MgTKT     TFLAFAD-YSKPAIR-LGALMNLPVFVYVYTHDSYQV-GG---DG-PTHQPYDQ--LPML
MjPTK1    SFSMFASGRAWEIIRNLVAYPKLVNIVATHAGITV-GE---DG-ASHQMCED--IAIM
BsTP      TSHSEQIPPPQNKGLLINMAGGTTKASMYLEALIDVTGQYTEYDLLPPLDPLNDKVIIRGL
N40KAT     KVGYEQIVYPDVASSSSFTVFGLYQQLLQSSSSAAV-----DIKASDLPQSGD-QVNK

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\*  
(SEQ ID NO: 12) Peptide A -> ASDLPQSGD-QVNK



Figure 8-2.

ScTKT1ct	RSLPNIQVWRPADGN-EVSAAYKNSLESKHTPSIIALSRQNLPOLEGS---	SIESASKGG	278
CpTKT7ct	RAMPNILTLPADGN-ETAGAYRAAVQNGERPSILVLARQKLPLPGT---	SIEGVSKGG	
EcTKT2ct	RLTPNFSTWRPCDQV-EAAVGVKLAVERHNGPTALILSRQNLQVVERTPD-QVKEIARGG		
BsTKTct	RAMPNLSLIRPADGN-ETAAAWKLAVQSTDHPTALVLTRQNLPTIDQTSEEALAGVEKGA		
MgTKT	RAIENVCVFRPCDEK-ETCAGFNYGLLSQDQTTVLVLTRQPLKSIDNTD--	SLKTL-KGG	
MjPTK1	RAIPNMVVIAPTYY-HTKNVIRTIAEYKG-PVYVRMPRRDTEIIYENEEETFEIGKKG		
BsTP	RLLINMAGEKPSQYVPEDGDAYVRASWFAQ-GSGRAFIGYSESMMRMG---	DYAEQVRFK	
N40KAT	DITQKYRTILDSTVV-ASQREYINSVKQKG-PISNYVVGYSMCEIK---	DIIRDQYN	

Peptide B -> TILDSTVV-ASQR (SEQ ID NO: 13)

ScTKT1ct	YVLQDVAN----	PDIILVATGSEVSLSVEAAKTLAAKNIKARVVSLPDFFTFDKQPLE-	332
CpTKT7ct	YVISDN\$RGGNSKPDVILIGTSELEIAARAGDELRKEGKKVRVSVLVCWELFAEQSEK-		
EcTKT2ct	YVLKDSGG----	KPDIILIIATGSEMEITLQAAEKLAGEGRNVRVSVLPSTDIFDAQDEE-	
BsTKTct	YVVSXSKN--E-TPDALLIASGSEVGLAIEAQAEAKENIDVSVVSMPSMDRFEKQSD-		
MgTKT	YILLDRKQ----	PDLIIAASGSEVQLAIEFEKVLTKQNVKVRILSVPNITLLLKQDEK-	
MjPTK1	ILVDG-----	EDLTIATGEEVPEALRAGEILKENGISAEIVEMATIKPIDEEIIKK	
BsTP	PISSSAG-----	QDIPLFYSDVSVNSKTAHPELAKKLANVMASADTVEQALRPQADGQ	
N40KAT	VQLIGTS-----	DKPYVYTDVLALNSN--LCDEKQKVAVEVIKNLLTNTLVLDLLG-	

ScTKT1ct	YRLSVLPDNPVI-MSVEVLATTCWGKYAH-----	QSFIDRFGASGKAPEVFKFFGFTP	385
CpTKT7ct	YRETVLP\$GVTARVSVEAGSTFGWERFIGP-KG--	KAVGIDRFGASAPAERLFKEFGITV	
EcTKT2ct	YRESVLPSNVAARVAVEAGIADYWKYVGL-KG--	AIVGMTGYGESAPADKLFPPFGFTA	
BsTKTct	YKNEVL\$PADVKKRLAIEMGSSFGWGKYTGL-EG--	DVLGIDRFGASAPGETIINEYGF\$V	
MgTKT	YLKSLFDANSSL-ITIEASSSYEWFCFKKY-VKNHAHLGAF\$FSGESDDGDKVYQKGFNL		
MjPTK1	SKDFVVTVEDHSIIGGLGGAVA\$VIASNGLNKKLLRIGINDV\$FGRSGKADELLKYYGLDG		
BsTP	YPQYLLPARHQV-YEALMQDYPIYSELAQIVNK--	PSNRV\$RLGPEVRT-WLKDAKQVLP	
N40KAT	-LGLTLPANKNG-IAHLAKSSNFYAQLSQ-----	QFDAKESEVRVLR\$VDFANKEV	

Peptide C -> SSNFYAQLSQ-----QFDAK (SEQ ID NO: 14)

ScTKT1ct	EGVAERAQKTIAFYKGDKLISPLKKAF	412	(SEQ ID NO: 5)
CpTKT7ct	EAVVA-AAKEIC-----		(SEQ ID NO: 6)
EcTKT2ct	ENIVAKAHKVLGVKGA-----		(SEQ ID NO: 7)
BsTKTct	PNVVNRVKALINK-----		(SEQ ID NO: 8)
MgTKT	ERLMKIFTSLRN-----		(SEQ ID NO: 9)
MjPTK1	ESIAKRIMEEMKKE-----		(SEQ ID NO: 10)
BsTP	EALGLTDVSSLAS-----		(SEQ ID NO: 11)
N40KAT	KNCAGVLRPFL-----		(SEQ ID NO: 4)